What is claimed is:

1. An isolated polynucleotide selected from the group consisting of:
   (a) a nucleic acid sequence having at least 85% sequence identity to presented as SEQ ID NO:1, or the complement thereof;
   (b) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an mHKCel polypeptide having at least 85% sequence identity to the amino acid sequence presented in Figure 3 (SEQ ID NO:3);
   (c) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an mHKCel polypeptide having at least 90% sequence identity to the amino acid sequence presented in Figure 3 (SEQ ID NO:3);
   (d) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an mHKCel polypeptide having at least 95% sequence identity to the amino acid sequence presented in Figure 3 (SEQ ID NO:3);
   (e) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an mHKCel polypeptide having the amino acid sequence presented in Figure 3 (SEQ ID NO:3);

wherein said isolated polynucleotide encodes a polypeptide having the biological activity of a cellulase and wherein the identity is determined by the CLUSTAL-W program in MacVector version 6.5, operated with default parameters, including an open gap penalty of 10.0, an extended gap penalty of 0.1, and a BLOSUM 30 similarity matrix.

2. An isolated polynucleotide selected from the group consisting of:
   (a) a nucleic acid sequence presented as SEQ ID NO:1, or the complement thereof;
   (b) a nucleic acid sequence that hybridizes, under high stringency conditions to the sequence presented as SEQ ID NO:1, or the complement or a fragment thereof,
   (c) a nucleic acid sequence presented as SEQ ID NO:2, or the complement thereof; and
   (d) a nucleic acid sequence that hybridizes, under high stringency conditions to the sequence presented as SEQ ID NO:2, or the complement or a fragment thereof,

wherein said isolated polynucleotide encodes a polypeptide having the biological activity of a cellulase and wherein hybridization is conducted at 42°C in 50% formamide, 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 µg/ml denatured carrier DNA followed by washing two times in 2X SSPE and 0.5% SDS at room temperature and two additional times in 0.1 SSPE and 0.5% SDS at 42°C.

3. The isolated nucleotide of claim 1 wherein the nucleotide is selected from the group mRNA, DNA, cDNA, genomic DNA, and an antisense analog thereof.

4. The isolated polynucleotide of Claim 3, wherein said polynucleotide is an RNA molecule.

5. The isolated polynucleotide of claim 1 encoding an enzyme having cellulase activity, wherein the enzyme is isolated from a *Trichoderma* source.

6. The isolated polynucleotide of Claim 5, wherein the enzyme is isolated from *Trichoderma reesei*.

7. An expression construct comprising a polynucleotide sequence encoding an amino acid sequence having cellulase activity and (i) having at least 85% sequence identity to the amino acid sequence presented in SEQ ID NO:3, or (ii) being capable of hybridizing to a probe designed to hybridize with the nucleotide sequence disclosed in Figure 2 under conditions of intermediate to high stringency, or (iii) being complementary to a nucleotide sequence having at least 85% sequence identity to a nucleotide sequence encoding the amino acid sequence presented in SEQ ID NO:3 wherein the identity is determined by the CLUSTAL-W program in MacVector version 6.5, operated with default parameters, including an open gap penalty of 10.0, an extended gap penalty of 0.1, and a BLOSUM 30 similarity matrix..

8. A expression vector comprising the polynucleotide of Claim 1.

9. A expression vector comprising an isolated polynucleotide of Claim 1, operably linked to control sequences recognized by a host cell transformed with the vector.

10. An expression vector according to Claim 9 comprising a regulatory polynucleotide sequence including a promoter sequence derived from a glucose isomerase gene of *Actinoplanes*, a signal sequence derived from a *Streptomyces* cellulase gene, and a polynucleotide sequence encoding a mHKCel cellulase.

11. A vector comprising the expression construct of Claim 8.

12. A host cell transformed with the vector of Claim 8.

13. The host cell of Claim 12, which is a prokaryotic cell.

14. The host cell of Claim 12, which is a eukaryotic cell.

15. A substantially purified mHKCel polypeptide with the biological activity of a cellulase, comprising a sequence selected from the group consisting of:

(a) an amino acid sequence having at least 85% sequence identity to the amino acid sequence presented in Figure 3 (SEQ ID NO:3);

(b) an amino acid sequence having at least 90% sequence identity to the amino acid sequence presented in Figure 3 (SEQ ID NO:3);

(c) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented in Figure 3 (SEQ ID NO:3);

(d) an amino acid sequence presented in Figure 3 (SEQ ID NO:3);

(e) a substantially purified biologically active fragment of the amino acid sequence presented as SEQ ID NO:3.

wherein the identity is determined by the CLUSTAL-W program in MacVector version 6.5, operated with default parameters, including an open gap penalty of 10.0, an extended gap penalty of 0.1, and a BLOSUM 30 similarity matrix.

16. The substantially purified mHKCel cellulase polypeptide or a derivative is provided which is obtainable from a *Bacillus*.

17. A method of producing a cellulase comprising the steps of:

(a) culturing the host cell according to claim 12 in a suitable culture medium under suitable conditions to produce the cellulase;

(b) obtaining said produced cellulase.

18. The method of Claim 17 wherein the host cell is a filamentous fungi or yeast cell.

19. The method of Claim 17 wherein the host cell is a bacterium.

20. The method of Claim 19 wherein the bacterium is a *Streptomyces*.

21. A purified enzyme having cellulase activity prepared by the method of Claim 17.

22. A recombinant host cell comprising a deletion or insertion or other alteration in the *mHKCel* gene which inactivates the gene and prevents mHKCel polypeptide production.

23. An antisense oligonucleotide complementary to a messenger RNA that encodes an mHKCel polypeptide having the sequence presented as SEQ ID NO:3, wherein upon exposure to a cellulase -producing host cell, said oligonucleotide decreases or inhibits the production of cellulase by said host cell.

24. The antisense oligonucleotide of Claim 23, wherein the host cell is a filamentous fungi.

25. A detergent composition, said composition comprising a polypeptide selected from the group consisting of:

(a) an amino acid sequence having at least 85% sequence identity to the amino acid sequence presented in Figure 3 (SEQ ID NO:3);
(b) an amino acid sequence having at least 90% sequence identity to the amino acid sequence presented in Figure 3 (SEQ ID NO:3);
(c) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented in Figure 3 (SEQ ID NO:3);
(d) an amino acid sequence presented in Figure 3 (SEQ ID NO:3);
(e) a substantially purified biologically active fragment of the amino acid sequence presented as SEQ ID NO:3

wherein the identity is determined by the CLUSTAL-W program in MacVector version 6.5, operated with default parameters, including an open gap penalty of 10.0, an extended gap penalty of 0.1, and a BLOSUM 30 similarity matrix.

26. A detergent composition comprising a surfactant and a cellulase according to Claim 15.

27. The detergent according to claim 25, wherein said detergent is a laundry detergent.

28. The detergent according to claim 25, wherein said detergent is a dish detergent.

29. A feed additive comprising a cellulase according to claim 15.

30. A method of treating wood pulp comprising contacting said wood pulp with a cellulase according to claim 15.

31. A method of converting biomass to sugars comprising contacting said biomass with a cellulase according to claim 15.

32. The method of Claim 31 further comprising the generation of high fructose corn-syrup

33. A method of producing ethanol, said method comprising the steps of:
(a) contacting a biomass composition with an enzymatic composition comprising mHKCel to yield a sugar solution;
(b) adding to the sugar solution a fermentative microorganism; and
(c) culturing the fermentative microorganism under conditions sufficient to produce ethanol,

33. A method of identifying novel enzymes comprising:
(a) isolating total microbial community DNA from an environment;
(b) constructing a genomic DNA library in *E.coli*;
(c) screening the library for expression of cellulase activity;

(d) identifying the cellulase gene in the cellulase-positive clone; and

(e) characterising the novel cellulase enzyme.

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